

DNA REPORT WRITING-GENERAL

A. SCOPE

The laboratory report must communicate both the analytical results and the conclusions of the examiner, conveying the essence of the expert testimony in court. The notes and other documentation must support the conclusions of the examiner. Decisions may be made by police officers, attorneys and the courts based on the report alone without examiner clarification, so the report should be able to stand alone. The report must contain the information required in the Laboratory Quality Assurance Manual and the FBI DNA Quality Assurance Audit Document.

Typical casework reporting should follow the recommended reporting statements, as appropriate. It is recognized that not every situation can be represented by these statements and that it may be necessary to modify the statements to accurately reflect the results.

B. REPORTING REQUIREMENTS

See Doc's [853](#) and [1817](#) for reporting requirements.

C. REPORTING STATEMENTS

C.1 EVIDENCE RECEIVED

Received from the Washoe County Sheriff's Office (WCSO) Evidence Section on **DATE**.

C.2 DESCRIPTION OF TECHNOLOGY:

C.2.1 QUANTITATION AND STR RESULTS ONLY:

PowerPlex 16 HS and WCSO database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit.

PCR amplification was completed using the PowerPlex® 16 HS PCR Amplification Kit.

Unless otherwise noted, all statistics represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the Washoe County Sheriff's Office Caucasian, African American and Hispanic population databases, with the most common of the three being reported. All conclusions assume individuals do not have an identical twin.

OR

PowerPlex 16 HS and NIST database

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(Reminder: calculations can be completed with 13 core loci only, Pentas not validated for use with NIST database)

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification was completed using the PowerPlex® 16 HS PCR Amplification Kit. Unless otherwise noted, all statistics represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases, with the most common of the four being reported. All conclusions assume individuals do not have an identical twin.

OR

GlobalFiler and NIST database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification was completed using the GlobalFiler® PCR Amplification Kit. Unless otherwise noted, all statistics represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases, with the most common of the four being reported. All conclusions assume individuals do not have an identical twin.

C.2.2 QUANTITATION AND Y STR RESULTS:

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification of the Y chromosome was completed using the AmpFℓSTR® Yfiler® PCR Amplification Kit.

All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

C.2.3 QUANTITATION, STR RESULTS, AND Y STR RESULTS:

PowerPlex 16 HS and WCSO database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification of the autosomal, X, and Y chromosomes was completed using the PowerPlex® 16 HS PCR Amplification Kit. PCR amplification of the Y chromosome was completed for the EVIDENCE and EVIDENCE and the reference sample from NAME using the AmpFℓSTR® Yfiler® PCR Amplification Kit. All statistics associated with autosomal STR results represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the Washoe County Sheriff's Office Caucasian, African American and Hispanic population databases, with the most common of the three being reported. All conclusions assume individuals do not have an identical twin.

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All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

OR

PowerPlex 16 HS and WCSO database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification of the autosomal, X, and Y chromosomes was completed using the PowerPlex® 16 HS PCR Amplification Kit. All statistics associated with autosomal STR results represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the Washoe County Sheriff's Office Caucasian, African American and Hispanic population databases, with the most common of the three being reported. All conclusions assume individuals do not have an identical twin. PCR amplification of the Y chromosome was completed for the EVIDENCE and EVIDENCE and the reference sample from NAME using the AmpFℓSTR® Yfiler® PCR Amplification Kit. All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

GlobalFiler and NIST database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification of the autosomal, X, and Y chromosomes was completed using the GlobalFiler® PCR Amplification Kit. PCR amplification of the Y chromosome was completed for the EVIDENCE and EVIDENCE and the reference sample from NAME using the AmpFℓSTR® Yfiler® PCR Amplification Kit. All statistics associated with autosomal STR results represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases, with the most common of the four being reported. All conclusions assume individuals do not have an identical twin. All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

OR

GlobalFiler and NIST database

PCR quantitation was completed using the Plexor® HY Human DNA Quantification Kit. PCR amplification of the autosomal, X, and Y chromosomes was completed using the GlobalFiler® PCR Amplification Kit. All statistics associated with autosomal STR results represent the expectation of observing the detected profile in a randomly selected unrelated individual and were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases, with the most common of the four being reported. All conclusions assume individuals do not have an

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identical twin. PCR amplification of the Y chromosome was completed for the EVIDENCE and EVIDENCE and the reference sample from NAME using the AmpF ℓ STR \textregistered Yfiler \textregistered PCR Amplification Kit. All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

C.2.4 QUANTITATION AND STR RESULTS FOR PARENTAGE:

PowerPlex 16 HS and WCSO database

PCR quantitation was completed using the Plexor \textregistered HY Human DNA Quantification Kit. PCR amplification was completed using the PowerPlex \textregistered 16 HS PCR Amplification Kit. All statistics were calculated using the Washoe County Sheriff's Office Caucasian, African American and Hispanic population databases.

OR (if for example Y-STR statistics were also calculated)

PCR quantitation was completed using the Plexor \textregistered HY Human DNA Quantification Kit. PCR amplification was completed using the PowerPlex \textregistered 16 HS PCR Amplification Kit. Parentage statistics were calculated using the Washoe County Sheriff's Office Caucasian, African American and Hispanic population databases. PCR amplification of the Y chromosome was completed using the AmpF ℓ STR \textregistered Yfiler \textregistered PCR Amplification Kit. All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

GlobalFiler and NIST database

PCR quantitation was completed using the Plexor \textregistered HY Human DNA Quantification Kit. PCR amplification was completed using the GlobalFiler \textregistered PCR Amplification Kit. All statistics were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases.

OR (if for example Y-STR statistics were also calculated)

PCR quantitation was completed using the Plexor \textregistered HY Human DNA Quantification Kit. PCR amplification was completed using the GlobalFiler \textregistered PCR Amplification Kit. Parentage statistics were calculated using the National Institute of Standards and Technology Caucasian, African American, Hispanic and Asian population databases. PCR amplification of the Y chromosome was completed using the AmpF ℓ STR \textregistered Yfiler \textregistered PCR Amplification Kit. All statistics associated with Y-STR results were generated using the combined data from all populations (African American, Asian, Caucasian, Hispanic, and Native American) in the US Y-STR Database.

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C.3 INTERPRETATION AND OPINION/CONCLUSIONS DOCUMENTATION

The following header will be used above the results section:

RESULTS AND CONCLUSIONS:

C.4 DISPOSITION OF EVIDENCE

Remember to include the appropriate sampling statement in all reports (e.g., a portion was removed....the entire swab was utilized, etc.)

C.4.1 Scenario Example: Removing a portion of the evidence and reference sample for DNA analysis. Entire cutting of evidence used for DNA analysis.

Reporting Statement: A cutting was removed from the **EVIDENCE** as **CUTTING NAME**. The **CUTTING NAME** and a portion of the **NAME** reference sample were utilized for DNA analysis. The remainder of the **NAME** reference sample will be placed in the Washoe County Sheriff's Office Evidence Section under **CONTROL #**.

C.4.2 Scenario Example: Removing a portion of the evidence and reference sample for DNA analysis. A portion of the cutting of evidence used for DNA analysis.

Reporting Statement: A cutting was removed from the **EVIDENCE** as **CUTTING NAME**. A portion of the **CUTTING NAME** and a portion of the **NAME** reference sample were utilized for DNA analysis. The remainder of the **CUTTING NAME** and **NAME** reference sample will be placed in the Washoe County Sheriff's Office Evidence Section under **CONTROL #**.

OR

Portions of the **EVIDENCE** swabs were utilized for DNA analysis.

C.4.3 Scenario Example: Evidence consumed and extracted material maintained.

Reporting Statement: The remainder of the extracted material from the **EVIDENCE** will be placed in the Washoe County Sheriff's Office Evidence Section under **CONTROL #**.

OR

The remaining extracted material from the **EVIDENCE** will be placed in the Washoe County Sheriff's Office Evidence Section under **CONTROL #**.

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C.4.4 Scenario Example: Extracted material consumed during analysis.

Reporting Statement: The extracted material from the **EVIDENCE** was consumed during analysis. Therefore, the extracted cutting / stain / swab from the **EVIDENCE** will be placed in the Washoe County Sheriff's Office Evidence Section under **CONTROL #**.

C.4.5 Scenario Example: When a portion of the evidence was removed / consumed.

Reporting Statement: Evidence remaining under **CONTROL #** was returned to the Washoe County Sheriff's Office Evidence Section.

C.4.6 Scenario Example: When the remaining portion of the evidence was put in a P# and brought to WCSO Evidence

Reporting Statement: The remaining portion of the EVIDENCE and EVIDENCE was placed in the Washoe County Sheriff's Office Evidence Section under PXXXX.

C.4.7 Scenario Example: When a portion of the evidence was forwarded to the DNA section for analysis

Reporting Statement: A portion of the EVIDENCE and EVIDENCE will be forwarded to the DNA Section for further examination.

C.4.8 Scenario Example: When 100% of the evidence was consumed.

Reporting Statement: **Control #** was returned to the Washoe County Sheriff's Office Evidence Section.

OR

The above listed control numbers were returned to the Washoe County Sheriff's Office Evidence Section.

C.4.9 Scenario Example: An item is forwarded to the Firearms Section after DNA analysis.

Reporting Statement: Evidence remaining under **CONTROL #** was returned to the WCSO Evidence Section and will be forwarded to the WCSO Firearms Section.

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C.4.10 Scenario Example: Remaining proficiency test samples will be kept in the Biology Unit (in an analyst's locker, the freezer, etc.) until the results have been reviewed.

Reporting Statement: Evidence remaining under **CONTROL** # will be retained in the Biology Unit pending evaluation of the analysis results.

C.5 LOW LEVEL RESULTS

C.5.1 Scenario Example: Low level results. No conclusions.

Reporting Statement: Due to a low level of DNA, no conclusions can be offered for the results obtained from **EVIDENCE**.

C.5.2 Scenario Example: Low level results and the reference sample can't be excluded but nor can they be included because there are not any loci suitable for statistics (the following statement can be used for casework analyzed with PowerPlex 16 HS, not GlobalFiler)

Reporting statement: Due to a low level of DNA, no conclusions can be offered for the comparison of the DNA profile obtained from the NAME reference sample and the partial DNA profile obtained from the EVIDENCE/DNA results obtained from the EVIDENCE.

C.5.3 Scenario Example: No results obtained during quantitation and after amplification.

Reporting Statement: No DNA results were obtained from **EVIDENCE**.

C.5.4 Scenario Example: Low level results obtained during quantitation but none detected after amplification.

Reporting Statement: No DNA typing results were obtained from **EVIDENCE**.

C.5.5 Scenario Example: No results obtained during quantitation and sample was concentrated prior to quantitation but not amplified.

Reporting Statement: No DNA was detected from the **EVIDENCE**.

C.5.6 Scenario Example: No DNA foreign to the source of the intimate sample(s) was obtained.

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Reporting Statement: No DNA foreign to **NAME** was detected from the following samples: **EVIDENCE**.

OR

No DNA foreign to **NAME** was obtained / detected from the **EVIDENCE**.

C.5.7 Scenario Example: DNA analysis is stopped after quantitation due to a limited quantity of DNA

Reporting Statement: Portions of the XXXX swabs were extracted and determined to contain a limited quantity of DNA. These items will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX. If analysis should become necessary, please contact the undersigned regarding evidence consumption.

C.5.8 Scenario Example: DNA analysis stopped after quantitation due to sample not containing any DNA (no DNA detected, extract not concentrated) and the sample was consumed (i.e. 100% of evidence placed in microtube)

Reporting Statement: The XXX swabs were extracted and determined to contain an insufficient quantity of DNA for further analysis. This item will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXX.

OR

No DNA was detected in the non-concentrated extract from the EVIDENCE. This item will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXX.

C.5.9 Scenario Example: DNA analysis is stopped after quantitation due to sample not containing any DNA (no DNA detected, extract not concentrated) and the sample was not consumed (i.e. 50% or less of sample placed in microtube)

Reporting Statement: The portions of the XXXX swabs that were extracted were determined to contain an insufficient quantity of DNA for further analysis. These items will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX. If analysis should

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become necessary, please contact the undersigned regarding evidence consumption.

OR

No DNA was detected in the non-concentrated extracts from the EVIDENCE. These items will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX. If analysis should become necessary, please contact the undersigned regarding evidence consumption.

C.5.10 Scenario Example: DNA analysis stopped after quantitation due to sample not containing any male DNA (extract was concentrated and no male DNA was detected)

Reporting Statement: No male DNA was detected in the portion of the XXXX swabs that was extracted. This item will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX. If analysis should become necessary, please contact the undersigned regarding evidence consumption.

C.5.11 Scenario Example: DNA analysis is stopped after quantitation due to a limited quantity of DNA; typical last sentence regarding evidence consumption not used because interpretable results were obtained from another swab/cutting of the same item OR the sample was consumed and gave a very low quant value or N/A

Reporting Statement: Portions of the XXXX swabs were extracted and determined to contain a limited quantity of DNA. These items will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX.

C.5.12 Scenario Example: DNA analysis is stopped after quantitation due to some samples containing no DNA (in concentrated extracts) and some samples containing a limited quantity of DNA

Reporting Statement: A portion of the XXXX swabs and a portion of the YYYY swabs were extracted and determined to contain no DNA and a limited quantity of DNA, respectively. These items will not be processed beyond the quantification step at this time. The remaining extracted material from these swabs will be placed in the Washoe County Sheriff's Office Evidence Section under PXXXXXX.

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If analysis should become necessary, please contact the undersigned regarding evidence consumption.

C.5.13 Scenario Example: Due to a low level of DNA, the number of contributors, and/or the nature of the mixture, no conclusions can be offered regardless of what's submitted for comparison/nor can the results be searched in the database

Reporting Statement: Additionally, this mixed DNA result is not suitable for DNA database searching purposes or comparison to DNA results from other cases and no conclusions can be offered should additional suspect reference samples become available.

OR

Additionally, these trace DNA results are not suitable for DNA database searching purposes or comparison to DNA results from other cases and no conclusions can be offered should additional suspect reference samples become available.

OR

Additionally, these trace DNA results are not suitable for DNA database searching purposes, for comparison to DNA results from other cases, or for comparison to additional suspect reference samples should they become available.

OR

The results obtained from the EVIDENCE indicate at least XXX sources of DNA. Due to a low level of DNA and the nature of this mixture, these results are not suitable for DNA database searching purposes and no conclusions can be offered should suspect reference samples become available.

C.5.14 Scenario Example: Low level, apparent single source DNA results that can be used to exclude an individual (with caution/some disclaimers)

Autosomal Reporting Statement: Low level DNA results (results at only X of the 15 tested locations) with no indication of a second contributor were obtained from the EVIDENCE. NAME is excluded as a source of this detected partial DNA profile.

Y Reporting Statement: Low level Y chromosomal DNA results (results at only X of the 17 tested locations) with no indication of a second contributor were obtained from the EVIDENCE. NAME and any of his male paternal biological

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relatives are excluded as a source of this detected Y chromosomal partial DNA profile.

C.6 REFERRING TO PREVIOUS REPORTS

C.6.1 Scenario Example: Need to compare newly developed profile to previously obtained results.

Reporting Statement: Please refer to previous reports under LXXXX-XX-X [Note: include submission number(s)], which include the analysis of X, Y, and Z.

OR

Reporting Statement: Please refer to a previous report under LXXXX-XX-X [Note: include submission number], which includes the analysis of X, Y, and Z.

C.7 IF REAGENT CONTROL IN P# CHECKED OUT FROM EVIDENCE

Received from the Washoe County Sheriff's Office Evidence Section on XXX

<u>CONTROL#</u>	<u>DESCRIPTION</u>
PXXXX	Extracted interior and exterior swabs, remaining extracted material from the exterior window swabs, and remaining corresponding reagent controls

One corresponding reagent control placed in PXXXX required further examination; all other items in this control number were not examined. Reagent controls are processed in duplicate. Low level DNA results were obtained from one of the reagent controls associated with this case. Due to a low level of DNA no conclusions can be offered for these low level DNA results. These results do not affect any conclusions and are isolated to this reagent control only.

C.8 IF A FAMILIAL RELATIONSHIP IS INDICATED IN THE MIXED DNA RESULTS

Reporting Statement: The DNA results obtained from the EVIDENCE indicate contributions from at least XX individuals. NAME 1 is excluded as a contributor to the mixed DNA results. Due to the possible relatedness of the contributors, no conclusions can be offered for the comparison of the NAME 2 reference sample to the mixed DNA results.

C.9 DNA BATCH REPORT EXAMPLE (TOP PORTION)

Refer to the previous report under L3633-14-0 for the primary examination results.

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The following items were received from the Biology Unit on 2/23/15 and subsequently utilized for DNA analysis

Description

Tubes containing the following:

Portion of the cigarette butt from the sidewalk labeled A1 cig (W279163)
Portion of the cigarette butt from the street labeled B1 cig (W279163)
Portion of the Christopher Price reference sample (W279161)
Portion of the Kelly Price reference sample (W279161)

RESULTS AND CONCLUSIONS:

Two different unknown male DNA profiles were obtained from the A1 and B1 cigarette butts...

OR

The following items were received from the Washoe County Sheriff's Office (WCSO) Biology Unit on 2/23/15 and subsequently utilized for DNA analysis

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